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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/318,443

DATE: 06/09/1999  
TIME: 13:48:50

Input Set: I318443.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Hemmati-Brivanlou, Ali
2      Weinstein, Daniel C.
3  <120> TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE
4      THEREOF
5  <130> FILE REFERENCE: 600-1-211 N
6  <140> CURRENT APPLICATION NUMBER: US/09/318,443
7  <141> CURRENT FILING DATE: 1999-05-25
8  <160> NUMBER OF SEQ ID NOS: 12
9  <170> SOFTWARE: PatentIn Ver. 2.0
10 <210> SEQ ID NO 1
11 <211> LENGTH: 1245
12 <212> TYPE: DNA
13 <213> ORGANISM: Xenopus laevis
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16      ttacggggagg aggatatgac caccgtggag ttccagacca gcgaagaagt ggatgtaacg 120
17      ccaacgtttg atacgatggg gctgagggaa gaccttctga gaggcattcta tgcttatgga 180
18      tttgagaaac catcggctat acaacagaag gcaatcaagc agatcatcaa aggaagggat 240
19      gtgatcgcac aatcacagtc tggtagagggc aaaacagcaa ctttttgtgt ttctgtgcta 300
20      cagtgtttgg atattcagat ccgtgaaacc caagccttga ttttagcacc caccaaagag 360
21      ttagcacggc aaattcagaa ggtgttgctt gctttggggg actacatgaa tgtgcagtgt 420
22      catgctgtga ttggaggcac aaatgttgga gaggatatcc gaaaattgga ttatgggcag 480
23      cacgttgttg ctggaacacc agggcgtggt tttgatatga ttcgacgcag aagttaaaga 540
24      actcggggcca ttaaaatggt agtgctggat gaagctgatg aaatgttgaa taagggtttc 600
25      aaggagcaaa tttatgatgt atacaggtat ctgcctccag caacacaagt ttgtttaatc 660
26      agtgctaccc tgccacatga aatcctggaa atgaccaata agtttatgac tgatcccatc 720
27      cgtatccttg tgaaacgtga tgagttgaca ctggaaggca tcaagcagtt ttttgtggca 780
28      gtggagagag aagagtggaa atttgatact ttgtgtgatt tatatgacac tttgactatt 840
29      acacaagctg taatcttctg caacacacaaa agaaaggtag attggttgac tgaaaaaatg 900
30      agagaagcaa atttcacagt ttctgcaatg catggtgata tgcccaaaaa ggagagagag 960
31      tcaatcatga aagaattccg atctggtgca agccgagtc tcatatcaac ggacgtcttg 1020
32      gcccgaggat tggatgtgcc acaggctctc ttgattatca actatgatct tcccaataac 1080
33      cgagaattgt acattcacag aattggccga tcaggaagat atggaagaaa ggggtgttgc 1140
34      attaaccttg tcaagaatga tgacatccgt attttaagag atattgagca gtactattcg 1200
35      acccagattg atgaaatgcc aatgaacgtt gctgatctta tttga 1245
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37 <211> LENGTH: 415
38 <212> TYPE: PRT
39 <213> ORGANISM: Xenopus laevis
40 <400> SEQUENCE: 2
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42      1 5 10 15
43      Ala Lys Arg Leu Leu Arg Glu Glu Asp Met Thr Thr Val Glu Phe Gln
44      20 25 30

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45      Thr Ser Glu Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu
46              35                      40                      45
47      Arg Glu Asp Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro
48              50                      55                      60
49      Ser Ala Ile Gln Gln Lys Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp
50              65                      70                      75                      80
51      Val Ile Ala Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys
52              85                      90                      95
53      Val Ser Val Leu Gln Cys Leu Asp Ile Gln Ile Arg Glu Thr Gln Ala
54              100                     105                     110
55      Leu Ile Leu Ala Pro Thr Lys Glu Leu Ala Arg Gln Ile Gln Lys Val
56              115                     120                     125
57      Leu Leu Ala Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile
58              130                     135                     140
59      Gly Gly Thr Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln
60              145                     150                     155                     160
61      His Val Val Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg
62              165                     170                     175
63      Arg Ser Leu Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala
64              180                     185                     190
65      Asp Glu Met Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr
66              195                     200                     205
67      Arg Tyr Leu Pro Pro Ala Thr Gln Val Cys Leu Ile Ser Ala Thr Leu
68              210                     215                     220
69      Pro His Glu Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile
70              225                     230                     235                     240
71      Arg Ile Leu Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln
72              245                     250                     255
73      Phe Phe Val Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys
74              260                     265                     270
75      Asp Leu Tyr Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn
76              275                     280                     285
77      Thr Lys Arg Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn
78              290                     295                     300
79      Phe Thr Val Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu
80              305                     310                     315                     320
81      Ser Ile Met Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser
82              325                     330                     335
83      Thr Asp Val Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile
84              340                     345                     350
85      Ile Asn Tyr Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile
86              355                     360                     365
87      Gly Arg Ser Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val
88              370                     375                     380
89      Lys Asn Asp Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser
90              385                     390                     395                     400
91      Thr Gln Ile Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile Glx
92              405                     410                     415

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93 &lt;210&gt; SEQ ID NO 3

94 &lt;211&gt; LENGTH: 532

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95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 3
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99   gccaccttca gtatctcagt cctccagtgt ttggatattc aggttcgtga aactcaagct 120
100  ttgatcttgg ctcccacaag agagttggct gtgcagatcc agaaggggct gcttgctctc 180
101  ggtgactaca tgaatgtcca gtgccatgcc tgcattggag gcaccaatgt tggcgaggac 240
102  atcaggaagc tggattacgg acagcatggt gttgcgggca ctccagggcg tgtttttgat 300
103  atgattcgtc gcagaagcct aaggacacgt gctatcaaaa tgttggtttt ggatgaagct 360
104  gatgaaatgt tgaataaagg tttcaaagag cagatttacg atgtatacag gtacctgcct 420
105  ccagccacac aggtgggttct catcagtgcc acgtgccac acgagattct ggagatgacc 480
106  aacaagttca tgaccgaccc aatccgcac ttggtgggaa ttctgcagc cc 532
107 <210> SEQ ID NO 4
108 <211> LENGTH: 177
109 <212> TYPE: PRT
110 <213> ORGANISM: Homo sapiens
111 <400> SEQUENCE: 4
112   Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala Gln Ser Gln Ser Gly
113   1           5           10          15
114   Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val Leu Gln Cys Leu Asp
115           20           25           30
116   Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu Ala Pro Thr Arg Glu
117           35           40           45
118   Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala Leu Gly Asp Tyr Met
119           50           55           60
120   Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr Asn Val Gly Glu Asp
121           65           70           75           80
122   Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val Ala Gly Thr Pro Gly
123           85           90           95
124   Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu Arg Thr Arg Ala Ile
125           100          105          110
126   Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Lys Gly Phe
127           115          120          125
128   Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu Pro Pro Ala Thr Gln
129           130          135          140
130   Val Val Leu Ile Ser Ala Thr Leu Pro His Glu Ile Leu Glu Met Thr
131           145          150          155          160
132   Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu Val Gly Ile Pro Ala
133           165          170          175
134   Ala
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136 <211> LENGTH: 1536
137 <212> TYPE: DNA
138 <213> ORGANISM: Homo sapiens
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141   cggactctga atcatggcga ccacggccac gatggcgacc tcgggctcgg cgcgaaagcg 120
142   gctgctcaaa gaggaagaca tgactaaagt ggaattcgag accagcgagg aggtggatgt 180
143   gacccccacg ttcgacacca tgggcctgcg ggaggacctg ctgcggggca tctacgctta 240
144   cggttttgaa aaaccatcag caatccagca acgagcaatc aagcagatca tcaaagggag 300

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145      agatgtcatc gcacagtctc agtccggcac agggaaaaaca gccaccttca gatatctcagt 360
146      cctccagtgt ttggatatcc aggttcgtga aactcaagct ttgatcttgg ctcccacaag 420
147      agagtgtggc gtgcagatcc agaaggggct gcttgctctc ggtgactaca tgaatgtcca 480
148      gtgccatgcc tgcattggag gcaccaatgt tggcgaggac atcaggaagc tggattacgg 540
149      acagcatggt gtcgcgggca ctccaggcg tgtttttgat atgattcgtc gcagaagcct 600
150      aaggacacgt gctatcaaaa tgttggtttt ggatgaagct gatgaaatgt tgaataaagg 660
151      tttcaaagag cagatttacg atgtatacag gtacctgcct tcagccacac aggtggttct 720
152      catcagtgcc acgtgccac acgagattct ggagatgacc aacaagttca tgaccgaccc 780
153      aatccgcac ttggtgaaac gtgatgaatt gactctggaa ggcatacagc aatttttctg 840
154      ggcagtggag agggaagagt ggaaatttga cactctgtgt gacctctacg acacactgac 900
155      catcactcag gcggtcatct tctgcaacac caaaagaaag gtggactggc tgacggagaa 960
156      aatgagggaa gccaaacttca ctgtatcctc aatgcatgga gacatgcccc agaaagagcg 1020
157      ggagtccatc atgaaggagt tccggtcggg cgccagcoga gtgcttattt ctacagatgt 1080
158      ctggggccagg gggttggatg tccctcaggt gtccctcctc attaactatg atctccctaa 1140
159      taacagagaa ttgtacatac acagaattgg gagatcaggt caatacggcc ggaagggtgt 1200
160      ggccattaac tttgtaaaga atgacgacat ccgcacctc agagatatcg agcagtacta 1260
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162      agtgggatga gggagactgt tcacctgctg tgtactcctg tttggaagta tttagatcca 1380
163      gattctactt aatgggggtt atatggactt tcttctcata aatggcctgc cgtctccctt 1440
164      cctttgaaga ggatatgggg attctgctct cttttcttat ttacatgtaa ataatacatt 1500
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&lt;210&gt; SEQ ID NO 6

&lt;211&gt; LENGTH: 411

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 6

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173      Leu Leu Lys Glu Glu Asp Met Thr Lys Val Glu Phe Glu Thr Ser Glu
174      . 20          25          30
175      Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp
176      35          40          45
177      Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile
178      50          55          60
179      Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala
180      65          70          75          80
181      Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val
182      85          90          95
183      Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu
184      100         105         110
185      Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala
186      115         120         125
187      Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr
188      130         135         140
189      Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val
190      145         150         155         160
191      Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu
192      165         170         175
193      Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met
194      180         185         190

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195      Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu
196              195                      200                      205
197      Pro Ser Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu
198              210                      215                      220
199      Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu
200      225                      230                      235                      240
201      Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val
202              245                      250                      255
203      Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr
204              260                      265                      270
205      Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg
206              275                      280                      285
207      Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val
208              290                      295                      300
209      Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met
210      305                      310                      315                      320
211      Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val
212              325                      330                      335
213      Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr
214              340                      345                      350
215      Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser
216              355                      360                      365
217      Gly Gln Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp
218              370                      375                      380
219      Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile
220      385                      390                      395                      400
221      Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile
222              405                      410
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224      <211> LENGTH: 1682
225      <212> TYPE: DNA
226      <213> ORGANISM: Homo sapiens
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229      cagcggcaca gcgaggtcgg cagcggcaca gcgaggtcgg cagcggcaca gcgaggtcgg 120
230      cagcggcagc gaggtcggca gcggcacagc gaggtcggca gcggcagcga ggtcggcagc 180
231      ggcgcgcgct gtgctcttcc gcggactctg aatcatggcg accacggcca cgatggcgac 240
232      ctcgggctcg gcgcgaaagc ggctgctcaa agaggaagac atgactaaag tgggaattcga 300
233      gaccagcgag gaggtggatg tgacccccac gttcgacacc atgggcctgc gggaggacct 360
234      gctgcggggc atctacgctt acggttttga aaaaccatca gcaatccagc aacgagcaat 420
235      caagcagatc atcaaaggga gagatgtcat cgcacagtct cagtccggca caggaaaaac 480
236      agccaccttc agtatctcag tctccagtg tttggatatt caggttcgtg aaactcaagc 540
237      tttgatcttg gtcgccaaa gagagttggc tgtgcagatc cagaaggggc tgcttgctct 600
238      cggtgactac atgaatgtcc agtgccatgc ctgcattgga ggcaccaatg ttggcgagga 660
239      catcaggaag ctggattacg gacagcatgt tgtcgcgggc actccagggc gtgtttttga 720
240      tatgattcgt cgcagaagcc taaggacacg tgctatcaaa atgttggttt tggatgaagc 780
241      tgatgaaatg ttgaataaag gtttcaaaga gcagatttac gatgtataca ggtacctgcc 840
242      tccagccaca caggtgggtc tcatcagtcg cacgctgcca cagcagattc tggagatgac 900
243      caacaagttc atgaccgacc caatccgcat cttgggtgaaa cgtgatgaat tgactctgga 960
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